



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stocco, Douglas M.  
Clark, Barbara J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF  
STEROIDOGENESIS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: U.S.A.  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown  
(B) FILING DATE: Concurrently Herewith  
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 33,732  
(C) REFERENCE/DOCKET NUMBER: 043375.0006/DLM

(ix) TELECOMMUNICATION INFORMATION:

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5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	GTCGACCCAC GCGTCCGCTC AGGACCTTGA AAGGCTCAGG AAGAACAACC CTTGAGCACC	60
	TCAGCACTCA GCATGTTTCT CGCTACGTTC AAGCTGTGTG CTGGAAGCTC CTATAGACAT	120
20	ATGCGGAATA TGAAAGGATT AAGGCACCAA GCTGTGCTGG CCATTGGCCA AGAGCTCAAC	180
	TGGAGAGCAC TGGGGGATTC CAGTCCCGGG TGGATGGGTC AAGTTCGACG TCGGAGCTCT	240
25	CTGCTTGGTT CTCAACTGGA AGCAACACTC TATAGTGACC AGGAGCTGTC CTACATCCAG	300
	CAGGGAGAGG TGGCTATGCA GAAGGCCTTG GGCATACTCA ACAACCAGGA AGGCTGGAAG	360
	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GTGCTAAGTA AGATGGTGCC AGATGTGGGC	420
30	AAGGTGTTTC GCTTGGAGGT GGTGGTAGAC CAGCCCATGG ACAGACTCTA TGAAGAACTT	480
	GTGGACCGCA TGGAGGCCAT GGGAGAGTGG AACCCAAATG TCAAGGAGAT CAAGGTCCTG	540
35	CAGAGGATTG GAAAAGACAC GGTCATCACT CATGAGCTGG CTGCGGCGGC AGCAGGCAAC	600

CTGGTG GGC CTCGAGACTT CGTGAGCGTG CGCTGTACCA AGCGCAGAGG TTCCACCTGT 660

GTGCTGGCAG GCATGGCCAC ACATTTTGGG GAGATGCCGG AGCAGAGTGG TGTCATCAGA 720

5 GCTGAACACG GCCCCACCTG CATGGTGCTT CATCCACTGG CTGGAAGTCC CTCCAAGACT 780

AAACTCACTT GGCTGCTCAG TATTGACCTG AAGGGGTGGC TGCCGAAGAC AATCATCAAC 840

CAGGTCCTAT CGCAGACCCA GATAGAGTTC GCCAACCACC TGCGCAAGCG CCTGGAAGCC 900

10 AGCCCTGCCT CTGAGGCCCA GTGTTAAGGA CTGTCCACCA CATTGACCTG CAAATCATTG 960

GAAGCTCTCA CAGGAAGCCT GCAAGTCTGT CCATCTTCAG CTAACAGCAT CGGGAGGGGT 1020

15 GGTAGTCAGG AGACACTAGG ACTGACTGGT AAAATCAGGA TCAGCAAAAT AGAAATGAGG 1080

CTTAGAATAA AAGTTCTCTA GTGTCTCCCA CTGCATAGCT GTGAAGGCTA AGGGATAAGT 1140

AGCTATGAAA CCTTTCATCT AGGCTTGTAT ATGCTGACCT AAAAGACACC AGCAGCTACG 1200

20 AACAGGGGAT GCTAAGGATC GGGAACTGTT GTCTTACCAG CTCCAAATGT CACTACCTGA 1260

AGGCAGTGTG CACACAAAGC AAGGTCTTGC CTAGGAAACT CTGTAAAAGT TCTCCTCTGT 1320

25 AAAAGGCCAG AACTTGAATG AACTACCTA CAAAGGGCCT TTCCAGAGTA TTCCAACCTT 1380

TCTCTGAGGA GAAATGAAAC CATCATTGTG CCGACTTCCC TACTAATCCC ATGACAATAA 1440

AGAACATACA TAAAAAAAAA AAAAAA 1466

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

- (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10	M	F	L	A	T	F	K	L	C	A	E	S	S	Y	R	H	
	Met	Phe	Leu	Ala	Thr	Phe	Lys	Leu	Cys	Ala	Gly	Ser	Ser	Tyr	Arg	His	
	1					5					10					15	
	M	R	N	M	L	G	L	R	H	Q	A	V	L	A	I	G	
	Met	Arg	Asn	Met	Lys	Gly	Leu	Arg	His	Gln	Ala	Val	Leu	Ala	Ile	Gly	
					20					25						30	
15	G	F	L	N	W	R	A	L	G	D	S	S	P	G	W	M	
	Gln	Glu	Leu	Asn	Trp	Arg	Ala	Leu	Gly	Asp	Ser	Ser	Pro	Gly	Trp	Met	
					35					40						45	
	G	Q	V	K	K	R	S	S	L	L	G	S	Q	L	E	A	
	Gly	Gln	Val	Arg	Arg	Arg	Ser	Ser	Leu	Leu	Gly	Ser	Gln	Leu	Glu	Ala	
					50					55						60	
20	T	L	Y	S	D	Q	E	L	S	Y	I	Q	Q	G	E	V	
	Thr	Leu	Tyr	Ser	Asp	Gln	Glu	Leu	Ser	Tyr	Ile	Gln	Gln	Gly	Glu	Val	
					65					70						80	
	A	M	Q	K	A	L	G	I	L	N	N	G	E	G	W	K	
	Ala	Met	Gln	Lys	Ala	Leu	Gly	Ile	Leu	Asn	Asn	Gln	Glu	Gly	Trp	Lys	
25					85					90						95	
	K	E	S	Q	Q	E	N	G	D	E	V	L	S	K	M	V	
	Lys	Glu	Ser	Gln	Gln	Glu	Asn	Gly	Asp	Glu	Val	Leu	Ser	Lys	Met	Val	
					100					105						110	
30	P	D	V	G	K	V	F	R	L	E	V	V	V	D	Q	P	
	Pro	Asp	Val	Gly	Lys	Val	Phe	Arg	Leu	Glu	Val	Val	Val	Asp	Gln	Pro	
					115					120						125	
	M	D	K	L	Y	E	E	L	V	D	K	M	E	A	M	G	
	Met	Asp	Arg	Leu	Tyr	Glu	Glu	Leu	Val	Asp	Arg	Met	Glu	Ala	Met	Gly	
					130					135						140	

35

E W N P N V K E I K V L Q R I G  
Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly  
145 150 155 160

K D T V I T H E L A A A A A G N  
Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn  
165 170 175

L V G P R D F V S V R C T K R R  
Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg  
180 185 190

G S T C V L A G M A T H F G E M  
Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met  
195 200 205

P E Q S G V I R A E H G P T C M  
Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met  
210 215 220

V L H P L A G S P S K T K L T W  
Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp  
225 230 235 240

L L S I D L K G W L P K T I I N  
Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn  
245 250 255

Q V L S G T Q I E F A N H L R K  
Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys  
260 265 270

R L E A S P A S E A Q C  
Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys  
275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



<sup>G S T C V L A G M A T H F G E M</sup>  
 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met  
 1                      5                      10                      15

<sup>P E Q</sup>  
 Pro Glu Gln

5

(2) INFORMATION FOR SEQ ID NO:6:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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<sup>N Q E G W K</sup>  
 Asn Gln Glu Gly Trp Lys  
 1                      5

(2) INFORMATION FOR SEQ ID NO:7:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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A E H G P T C M V  
Ala Glu His Gly Pro Thr Cys Met Val

1

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5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

I L N N Q E G W K K E  
Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu  
1 5 10

20 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

30

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(3, 12, 15, 18)

(D) OTHER INFORMATION: /mod\_base= OTHER

35 /note= "N = (A or C or G or T/U) or (unknown or other)"



(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: 6

(D) OTHER INFORMATION: /mod\_base= OTHER

5 /note= "R = A or G"

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(9, 21)

10 (D) OTHER INFORMATION: /mod\_base= OTHER

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 GCNGARCAYG GNCCNACNTG YATGG

25

(2) INFORMATION FOR SEQ ID NO:10:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

30 (A) NAME/KEY: modified\_base

(B) LOCATION: one-of(5, 17)

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "R = A or G"

35 (ix) FEATURE:

(A) NAME/KEY: modified\_base  
(B) LOCATION: one-of(8, 11, 14, 23)  
(D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = (A or C or G or T/U) or (unknown or other)"

5

(ix) FEATURE:

(A) NAME/KEY: modified\_base  
(B) LOCATION: 20  
(D) OTHER INFORMATION: /mod\_base= OTHER

10

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATRCANGT NGGNC CRTGY TCNGC

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

(A) NAME/KEY: modified\_base  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /mod\_base= OTHER

30

/note= "Y = C or T/U"

(ix) FEATURE:

(A) NAME/KEY: modified\_base

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(B) LOCATION: one-of(6, 9)

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "R = A or G"

5 (ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: 12

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "N = (A or C or G or T/U) or (unknown or other)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAYCARCARG GNTGGAA

17

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCANCCYT CYTGRTT

17

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10	AACCAGGAAG GCTGGAAGAA GGAAAGCCAG CAGGAGAACG GGGACGAAGT GCTAAGTAAG	60
	ATGGTGCCAG ATGTGGGCAA GGTGTTTCGC TTGGAGGTGG TGGTAGACCA GCCCATGGAC	120
	AGACTCTATG AAGAACTTGT GGACCGCATG GAGGCCATGG GAGAGTGGAA CCCAAATGTC	180
15	AAGGAGATCA AGGTCCTGCA GAGGATTGGA AAAGACACGG TCATCACTCA TGAGCTGGCT	240
	GCGGCGGCAG CAGGCAACCT GGTGGGGCCT CGAGACTTCG TGAGCGTGCG CTGTACCAAG	300
20	CGCAGAGGTT CCACCTGTGT GCTGGCAGGC ATGGCCACAC ATTTTGGGGA GATGCCGGAG	360
	CAGAGTGGTG TCATCAGAGC TGAACACGGC CCCACCTGCA T	401

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "RNA"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	GUCGACCCAC GCGUCCGCUC AGGACCUUGA AAGGCUCAGG AAGAACAACC CUUGAGCACC	60
5	UCAGCACUCA GCAUGUUCU CGCUACGUUC AAGCUGUGUG CUGGAAGCUC CUAUAGACAU	120
	AUGCGGAAUA UGAAAGGAUU AAGGCACCAA GCUGUGCUGG CCAUUGGCCA AGAGCUCAAC	180
	UGGAGAGCAC UGGGGGAUUC CAGUCCCGGG UGGAUGGGUC AAGUUCGACG UCGGAGCUCU	240
10	CUGCUUGGUU CUCAACUGGA AGCAACACUC UAUAGUGACC AGGAGCUGUC CUACAUCAG	300
	CAGGGAGAGG UGGCUAUGCA GAAGGCTUUG GGCAUACUCA ACAACCAGGA AGGCUGGAAG	360
15	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GUGCUAAGUA AGAUGGUGCC AGAUGUGGGC	420
	AAGGUGUUUC GCUUGGAGGU GGUGGUAGAC CAGCCCAUGG ACAGACUCUA UGAAGAACUU	480
	GUGGACCGCA UGGAGGCCAU GGGAGAGUGG AACCCTAAUG UCAAGGAGAU CAAGGUCCUG	540
20	CAGAGGAUUG GAAAAGACAC GGUCAUCACU CAUGAGCUGG CUGCGGCGGC AGCAGGCAAC	600
	CUGGUGGGGC CUCGAGACUU CGUGAGCGUG CGCUGUACCA AGCGCAGAGG UUCCACCUGU	660
25	GUGCUGGCAG GCAUGGCCAC ACAUUUUGGG GAGAUGCCGG AGCAGAGUGG UGUCAUCAGA	720
	GCUGAACACG GCCCCACTUG CAUGGUGCUU CAUCCACUGG CUGGAAGUCC CUCCAAGACU	780
	AAACUCACUU GGCUGCUCAG UAUUGACCUG AAGGGGUGGC UGCCGAAGAC AAUCAUCAAC	840
30	CAGGUCCUUAU CGCAGACCCA GAUAGAGUUC GCCAACCACC UGCGCAAGCG CCUGGAAGCC	900
	AGCCUGCCU CUGAGGCCCA GUGUUAAGGA CUGUCCACCA CAUUGACCUG CAAUCAUUG	960
35	GAAGCUCUCA CAGGAAGCCU GCAAGUCUGU CCAUCUUCAG CUAACAGCAU CGGGAGGGGU	1020

	GGUAGUCAGG AGACACUAGG ACUGACUGGU AAAAUCAGGA UCAGCAAAAU AGAAAUGAGG	1080
	CUUAGAAUAA AAGUUCUCUA GUGUCUCCCA CUGCAUAGCU GUGAAGGCUA AGGGUAUAGU	1140
5	AGCUAUGAAA CCUUUCAUCU AGGCUUGUAU AUGCUGACCU AAAAGACACC AGCAGCUACG	1200
	AACAGGGGAU GCUAAGGAUC GGGAACUGUU GUCUUACCAG CUCCAAAUGU CACUACCUGA	1260
	AGGCAGUGUG CACACAAAGC AAGGUCUUGC CUAGGAAACU CUGUAAAAGU UCUCCUCUGU	1320
10	AAAAGGCCAG AACUUGAUG AAACUACCUA CAAAGGGCCU UCCAGAGUA UUCAACUUU	1380
	UCUCUGAGGA GAAUGAAAC CAUCAUUGUG CCGACUCCCC UACUAAUCCC AUGACAAUAA	1440
15	AGAACAUACA UAAAAAAAAA AAAAAA	1466

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

25 (ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:15:

30	267 GTGGATTAAC CAGGTTCTGGC GCGGAGCTC TCTACTCGGT TCTCGGCTGG AAGAGACTCT	326
	327 CTACAGTGAC CAGGAGCTGG CCTATCTCCA GCAGGGGGAG GAGGCCATGC AGAAGGCCTT	386
	387 GGGCATCCTT AGCAACCAAG AGGGCTGGAA GAAGGAGAGT CAGCAGGACA ATGGGGACAA	446
	447 AGTGATGAGT AAAGTGGTCC CAGATGTGGG CAAGGTGTTC CGGCTGGAGG TCGTGGTGGA	506
35	507 CCAGCCCATG GAGAGGCTCT ATGAAGAGCT CGTGGAGCGC ATGGAAGCAA TGGGGGAGTG	566

567 GAACCCCAAT GTCAAGGAGA TCAAGGTCCT GCAGAAGATC GGAAAAGATA CATTTCATTAC 626  
 627 TCACGAGCTG GCTGCCGAGG CAGCAGGAAA CCTGGTG GGGG CCCCCTGACT TTGTGAGCGT 686  
 687 GCGCTGTGCC AAGCGCCGAG GCTCCACCTG TGTGCTGGCT GGCATGGACA CAGACTTCGG 746  
 747 GAACATGCCT GAGCAGAAGG GTGTCATCAG GGCGGAGCAC GGTCCCACCTT GCATGGTGCT 806  
 5 807 TCACCCGTTG GCTGGAAGTC CCTCTAAGAC CAAACTTACG TGGCTACTCA GCATCGACCT 866  
 867 CAAGGGGTGG CTGCCCAAGA GCATCATCAA CCAGGTCCTG TCCCAGACCC AGGTGGATTT 926  
 927 TGCCAACCAC CTGCGCAAGC GCCTGGAGTC CCACCCTGCC TCTGAAGCCA GGTGTTGAAG 986  
 987 AC 988

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

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(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

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(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:16:

127 ATGCTGCTAG CGACATTCAA GCTGTGCGCT GGGAGCTCCT ACAGACACAT GCGCAACATG 186  
 25 187 AAGGGGCTGA GGCAACAGGC TGTGATGGCC ATCAGCCAGG AGCTGAACCG GAGGGCCCTG 246  
 247 GGGGGCCCCA CCCC 260

(2) INFORMATION FOR SEQ ID NO:17:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

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(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:17:

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1051 ACTGGAAGCC TGCAAGTCT 1069

(2) INFORMATION FOR SEQ ID NO:18:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

15

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

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SEQUENCE DESCRIPTION: SEQ ID NO:18:

1	MLLATFKLCA GSSYRHRNM KGLRQQAVMA ISQELNRRAL GGPTPSTWIN	50
51	QVRRRSSLLG SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKES	100
101	QQDNGDKVMS KVVDPVGKVF RLEVVDQPM ERLYEELVER MEAMGEWNP	150
25	151 VKEIKVLQKI GKDTFITHL AABAAGNLVG PRDFVSVRCA KRGSTCVLA	200
	201 GMATDFGNMP EQKGVIKAEH GPTCMVLHPL AGSPSKTKLT WLLSIDLKGW	250
	251 LPKSIINQVL SQTQVDFANHL RKRLESHPA SEARC	285

(2) INFORMATION FOR SEQ ID NO:19:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

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(D) TOPOLOGY:



(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:19:

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agaacaccag gtccaggctg cagctgcggg actcagaggc gaacgttgag gggctcagga 60  
aggacgaaga accacccttg agagaagagg cagcagcagc gcggcagcag cagcggcagc 120  
gacccccacca ctgccacatt tgccaggaaa caATGCTGCT AGCGACATTC AAGCTGTGCG 180  
CTGGGAGCTC CTACAGACAC ATGCGCAACA TGAAGGGGCT GAGGCAACAG GCTGTGATGG 240  
CCATCAGCCA GGAGCTGAAC CGGAGGGCCC TGGGGGGCCC CACCCTAGC ACGTGGATTA 300  
ACCAGGTTCTG GCGGCGGAGC TCTCTACTCG GTTCTCGGCT GGAAGAGACT CTCTACAGTG 360  
ACCAGGAGCT GGCCTATCTC CAGCAGGGGG AGGAGGCCAT GCAGAAGGCC TTGGGCATCC 420  
TTAGCAACCA AGAGGGCTGG AAGAAGGAGA GTCAGCAGGA CAATGGGGAC AAAGTGATGA 480  
GTAAAGTGGT CCCAGATGTG GGCAAGGTGT TCCGGCTGGA GGTCGTGGTG GACCAGCCCA 540  
TGGAGAGGCT CTATGAAGAG CTCGTGGAGC GCATGGAAGC AATGGGGGAG TGGAAACCCCA 600  
ATGTCAAGGA GATCAAGGTC CTGCAGAAGA TCGGAAAAGA TACATTTCATT ACTCACGAGC 660  
TGGCTGCCGA GGCAGCAGGA AACCTGGTGG GGCCCCGTGA CTTTGTGAGC GTGCGCTGTG 720  
CCAAGCGCCG AGGCTCCACC TGTGTGCTGG CTGGCATGGC CACAGACTTC GGGAACATGC 780  
CTGAGCAGAA GGGTGTCTATC AGGGCGGAGC ACGGTCCCAC TTGCATGGTG CTTACCCCGT 840  
TGGCTGGAAG TCCCTCTAAG ACCAAACTTA CGTGGCTACT CAGCATCGAC CTCAAGGGGT 900  
GGCTGCCCAA GAGCATCATC AACCAGGTCC TGTCCCAGAC CCAGGTGGAT TTTGCCAACC 960  
ACCTGCGCAA GCGCCTGGAG TCCCACCCTG CCTCTGAAGC CAGGTGTTGA agaccagcct 1020  
gctgttccca actgtgccca gctgcactgg tacacacgct catcaggaga atccctactg 1080  
gaagcctgca agtctaagat ctccatctgg tgacagtggg atgggtgggg ttcgtgttta 1140  
gagtatgaca ctaggattca gattggtgaa agtttttagt accaagaaaa cagggatgag 1200  
ctcttggatt aaaaggtaac ttcattcact gattagctat gacatgaggg ttcaggcccg 1260  
ctaaaaataa ttgtaaaact tttttctggt gcccttatgt acccacctaa aaccatcttt 1320  
aaaatgctag tggctgatat ggggtgtggg gatgctaacc acagggcctg agaagtcttg 1380  
ctttatgggc tcaagaatgc catgcgctgg cagtacatgt gcacaaagca gaatctcaga 1440  
gggtctctctg cagccctctg ctctctccgg ccgctgcaca gcaacaccac agaacaagca 1500  
gcaccccaaca gtgggtgcct tccagaaata tagtccaagc tttctctgtg gaaaaagaca 1560  
aaactcatta gtagacatgt ttcctattg ctttcatagg caccagtcag aataaagaat 1620  
cataattcac acaaaaaaaaa a 1641